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SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.
THE UNIVERSITY OF TOKYO

<120> METHODS OF DETECTING METHYL TRANSFERASE ACTIVITY AND METHODS OF
SCREENING FOR METHYL TRANSFERASE ACTIVITY MODULATORS

<130> ONC-A0310P

<150> US 60/538,658

<151> 2004-01-23

<160> 55

<170> PatentIn version 3.3

<210> 1

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2 / 3 6

acaacagcct caagatcatc ag

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3 / 36

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4 / 3 6

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6 / 3 6

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7 / 3 6

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caaacaggaa ccaagaacaa gtc

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8 / 36

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9 / 36

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1 4 / 3 6

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1 5 / 3 6

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17/36

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18 / 36

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ggtaagatca aaggg

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ccctttggcc ttacc

15

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19 / 36

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ggtaaggcca aaggg

15

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<211> 29

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mutant-type ZNFN3A1.

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cggaattctg gcgtcgtctg cgaccgctg

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<212> DNA

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2 2 / 3 6

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agcgggcctg gtaccaaatt tgtg

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<211> 24

<212> DNA

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<223> An artificially synthesized primer sequence to amplify the
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ccgggatgct agcgcatтта cagc

24

<210> 48

<211> 55

24 / 36

<212> DNA

<213> Artificial

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<223> An artificially synthesized oligonucleotide sequence for plasmids
expressing siRNA to ZNFN3A1

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caccaacatc taccagctga aggtgttcaa gagacacctt cagctggtag atgtt 55

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<213> Artificial

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25 / 36

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Met Glu Pro Leu Lys Val

1

5

gaa aag ttc gca acc gcc aac agg gga aac ggg ctg cgc gcc gtg acc 161

Glu Lys Phe Ala Thr Ala Asn Arg Gly Asn Gly Leu Arg Ala Val Thr

10

15

20

ccg ctg cgc ccc gga gag cta ctc ttc cgc tcg gat ccc ttg gcg tac 209

Pro Leu Arg Pro Gly Glu Leu Leu Phe Arg Ser Asp Pro Leu Ala Tyr

25

30

35

acg gtg tgc aag ggg agt cgt ggc gtc gtc tgc gac cgc tgc ctt ctc 257

Thr Val Cys Lys Gly Ser Arg Gly Val Val Cys Asp Arg Cys Leu Leu

40

45

50

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ggg aag gaa aag ctg atg cga tgc tct cag tgc cgc gtc gcc aaa tac 305
 Gly Lys Glu Lys Leu Met Arg Cys Ser Gln Cys Arg Val Ala Lys Tyr
 55 60 65 70

tgt agt gct aag tgt cag aaa aaa gct tgg cca gac cac aag cgg gaa 353
 Cys Ser Ala Lys Cys Gln Lys Lys Ala Trp Pro Asp His Lys Arg Glu
 75 80 85

tgc aaa tgc ctt aaa agc tgc aaa ccc aga tat cct cca gac tcc gtt 401
 Cys Lys Cys Leu Lys Ser Cys Lys Pro Arg Tyr Pro Pro Asp Ser Val
 90 95 100

cga ctt ctt ggc aga gtt gtc ttc aaa ctt atg gat gga gca cct tca 449
 Arg Leu Leu Gly Arg Val Val Phe Lys Leu Met Asp Gly Ala Pro Ser
 105 110 115

gaa tca gag aag ctt tac tca ttt tat gat ctg gag tca aat att aac 497
 Glu Ser Glu Lys Leu Tyr Ser Phe Tyr Asp Leu Glu Ser Asn Ile Asn
 120 125 130

aaa ctg act gaa gat aag aaa gag ggc ctc agg caa ctc gta atg aca 545
 Lys Leu Thr Glu Asp Lys Lys Glu Gly Leu Arg Gln Leu Val Met Thr
 135 140 145 150

ttt caa cat ttc atg aga gaa gaa ata cag gat gcc tct cag ctg cca 593

27 / 36

Phe Gln His Phe Met Arg Glu Glu Ile Gln Asp Ala Ser Gln Leu Pro

155

160

165

cct gcc ttt gac ctt ttt gaa gcc ttt gca aaa gtg atc tgc aac tct 641

Pro Ala Phe Asp Leu Phe Glu Ala Phe Ala Lys Val Ile Cys Asn Ser

170

175

180

ttc acc atc tgt aat gcg gag atg cag gaa gtt ggt gtt ggc cta tat 689

Phe Thr Ile Cys Asn Ala Glu Met Gln Glu Val Gly Val Gly Leu Tyr

185

190

195

ccc agt atc tct ttg ctc aat cac agc tgt gac ccc aac tgt tcg att 737

Pro Ser Ile Ser Leu Leu Asn His Ser Cys Asp Pro Asn Cys Ser Ile

200

205

210

gtg ttc aat ggg ccc cac ctc tta ctg cga gca gtc cga gac atc gag 785

Val Phe Asn Gly Pro His Leu Leu Leu Arg Ala Val Arg Asp Ile Glu

215

220

225

230

gtg gga gag gag ctc acc atc tgc tac ctg gat atg ctg atg acc agt 833

Val Gly Glu Glu Leu Thr Ile Cys Tyr Leu Asp Met Leu Met Thr Ser

235

240

245

gag gag cgc cgg aag cag ctg agg gac cag tac tgc ttt gaa tgt gac 881

Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln Tyr Cys Phe Glu Cys Asp

250

255

260

28 / 36

tgt ttc cgt tgc caa acc cag gac aag gat gct gat atg cta act ggt 929

Cys Phe Arg Cys Gln Thr Gln Asp Lys Asp Ala Asp Met Leu Thr Gly

265

270

275

gat gag caa gta tgg aag gaa gtt caa gaa tcc ctg aaa aaa att gaa 977

Asp Glu Gln Val Trp Lys Glu Val Gln Glu Ser Leu Lys Lys Ile Glu

280

285

290

gaa ctg aag gca cac tgg aag tgg gag cag gtt ctg gcc atg tgc cag 1025

Glu Leu Lys Ala His Trp Lys Trp Glu Gln Val Leu Ala Met Cys Gln

295

300

305

310

gcg atc ata agc agc aat tct gaa cgg ctt ccc gat atc aac atc tac 1073

Ala Ile Ile Ser Ser Asn Ser Glu Arg Leu Pro Asp Ile Asn Ile Tyr

315

320

325

cag ctg aag gtg ctc gac tgc gcc atg gat gcc tgc atc aac ctc ggc 1121

Gln Leu Lys Val Leu Asp Cys Ala Met Asp Ala Cys Ile Asn Leu Gly

330

335

340

ctg ttg gag gaa gcc ttg ttc tat ggt act cgg acc atg gag cca tac 1169

Leu Leu Glu Glu Ala Leu Phe Tyr Gly Thr Arg Thr Met Glu Pro Tyr

345

350

355

agg att ttt ttc cca gga agc cat ccc gtc aga ggg gtt caa gtg atg 1217

29 / 36

Arg Ile Phe Phe Pro Gly Ser His Pro Val Arg Gly Val Gln Val Met

360

365

370

aaa gtt ggc aaa ctg cag cta cat caa ggc atg ttt ccc caa gca atg 1265

Lys Val Gly Lys Leu Gln Leu His Gln Gly Met Phe Pro Gln Ala Met

375

380

385

390

aag aat ctg aga ctg gct ttt gat att atg aga gtg aca cat ggc aga 1313

Lys Asn Leu Arg Leu Ala Phe Asp Ile Met Arg Val Thr His Gly Arg

395

400

405

gaa cac agc ctg att gaa gat ttg att cta ctt tta gaa gaa tgc gac 1361

Glu His Ser Leu Ile Glu Asp Leu Ile Leu Leu Leu Glu Glu Cys Asp

410

415

420

gcc aac atc aga gca tcc taa gggaacgcag tcagagggaa atacggcgtg 1412

Ala Asn Ile Arg Ala Ser

425

tgtctttgtt gaatgcctta ttgaggtcac acactctatg ctttggttagc tgtgtgaacc 1472

tctcttattg gaaattctgt tccgtgtttg tgtaggtaaa taaaggcaga catggtttgc 1532

aaaccacaag aatcattagt tgtagagaag cagcattata ataaattcaa aacatttggt 1592

tgaggatgcc aaaaaaaaaa aaaaaaaaaa 1622

30 / 36

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<211> 428

<212> PRT

<213> Homo sapiens

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Gly Leu Arg Ala Val Thr Pro Leu Arg Pro Gly Glu Leu Leu Phe Arg

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Ser Asp Pro Leu Ala Tyr Thr Val Cys Lys Gly Ser Arg Gly Val Val

35 40 45

Cys Asp Arg Cys Leu Leu Gly Lys Glu Lys Leu Met Arg Cys Ser Gln

50 55 60

Cys Arg Val Ala Lys Tyr Cys Ser Ala Lys Cys Gln Lys Lys Ala Trp

3 1 / 3 6

65 70 75 80

Pro Asp His Lys Arg Glu Cys Lys Cys Leu Lys Ser Cys Lys Pro Arg
 85 90 95

Tyr Pro Pro Asp Ser Val Arg Leu Leu Gly Arg Val Val Phe Lys Leu
 100 105 110

Met Asp Gly Ala Pro Ser Glu Ser Glu Lys Leu Tyr Ser Phe Tyr Asp
 115 120 125

Leu Glu Ser Asn Ile Asn Lys Leu Thr Glu Asp Lys Lys Glu Gly Leu
 130 135 140

Arg Gln Leu Val Met Thr Phe Gln His Phe Met Arg Glu Glu Ile Gln
145 150 155 160

Asp Ala Ser Gln Leu Pro Pro Ala Phe Asp Leu Phe Glu Ala Phe Ala
 165 170 175

32 / 36

Lys Val Ile Cys Asn Ser Phe Thr Ile Cys Asn Ala Glu Met Gln Glu

180

185

190

Val Gly Val Gly Leu Tyr Pro Ser Ile Ser Leu Leu Asn His Ser Cys

195

200

205

Asp Pro Asn Cys Ser Ile Val Phe Asn Gly Pro His Leu Leu Leu Arg

210

215

220

Ala Val Arg Asp Ile Glu Val Gly Glu Glu Leu Thr Ile Cys Tyr Leu

225

230

235

240

Asp Met Leu Met Thr Ser Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln

245

250

255

Tyr Cys Phe Glu Cys Asp Cys Phe Arg Cys Gln Thr Gln Asp Lys Asp

260

265

270

Ala Asp Met Leu Thr Gly Asp Glu Gln Val Trp Lys Glu Val Gln Glu

3 3 / 3 6

275

280

285

Ser Leu Lys Lys Ile Glu Glu Leu Lys Ala His Trp Lys Trp Glu Gln

290

295

300

Val Leu Ala Met Cys Gln Ala Ile Ile Ser Ser Asn Ser Glu Arg Leu

305

310

315

320

Pro Asp Ile Asn Ile Tyr Gln Leu Lys Val Leu Asp Cys Ala Met Asp

325

330

335

Ala Cys Ile Asn Leu Gly Leu Leu Glu Glu Ala Leu Phe Tyr Gly Thr

340

345

350

Arg Thr Met Glu Pro Tyr Arg Ile Phe Phe Pro Gly Ser His Pro Val

355

360

365

Arg Gly Val Gln Val Met Lys Val Gly Lys Leu Gln Leu His Gln Gly

370

375

380

3 4 / 3 6

Met Phe Pro Gln Ala Met Lys Asn Leu Arg Leu Ala Phe Asp Ile Met

385

390

395

400

Arg Val Thr His Gly Arg Glu His Ser Leu Ile Glu Asp Leu Ile Leu

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415

Leu Leu Glu Glu Cys Asp Ala Asn Ile Arg Ala Ser

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425

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<213> Homo sapiens

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Asn His Ser Cys Asp Pro Asn

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<210> 53

<211> 8

3 5 / 3 6

<212> PRT

<213> Homo sapiens

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Gly Glu Glu Leu Thr Ile Cys Tyr

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Asn His Ser Cys Xaa Xaa Asn

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3 6 / 3 6

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Gly Glu Glu Leu Xaa Xaa Xaa Tyr

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